

13:42:29 2004

48-09-424-686f-10.res

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 0 1250 1260 1270 1280 1290
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 :TACGTGCCACTCTGGGTCACTCAGGACGCCAGGCCAGGCCTGAGTCGGAAAGCTCC
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Sequence Name	Description	Init. Opt.	Length	Score	Score S:
*** 7 standard deviations above mean ****					
1. US-08-851-843A-2 Sequence 224, Application 4015 2532 3716					
1. US-09-424-686F-10 (1-3824) US-08-851-843A-2 Sequence 224, Application US/08851843A					
Initial Score = 2532 Optimized Score = 3716 Significance = 3716	Residue Identity = 94% Matches = 3797 Mismatches = 3797	Gaps = 218 Conservative Substitutions = 218			
GTTCAGGCAGGCTCGTCCCTGCTGGAAAGCCCTGGGACCTGGGATGCC GCAGGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGC X 10 20 30 40 50 60					
CTCCCCGCTGCCAGGCCGCTGCCAGGCCACTACCGGAGGGCTGGCTGGCA CTCCCCGCTGCCAGGCCGCTGCCAGGCCACTACCGGAGGGCTGGCTGGCA 70 80 90 100 110 120 130 140 150 160 170 180 190 200					
TGCGGGCCTGGGGCCAGGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGC TGCGGGCCTGGGGCCAGGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGC 140 150 160 170 180 190 200					
CCCAGTGCTGGTGTGGCTGGCTGGGACGGCACGGCGCCCTGGGAGGGCT CCCAGTGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGC 210 220 230 240 250 260 270 280					
GCCCTGAAGGAGCTGGCTGGCCAGGTGCTGGAGGGCTGTGGAGGGCT GCCCTGAAGGAGCTGGCTGGCCAGGTGCTGGAGGGCTGTGGAGGGCT 210 220 230 240 250 260 270 280					
370 380 390 400 410 420 GCTTCGGCTGCTGGAGGGCTTCACCCACAGGTGGCAGGGCT GCTTCGGCTGCTGGAGGGCTTCACCCACAGGTGGCAGGGCT 360 370 380 390 400 410 420					
440 450 460 470 480 490 500 CCAACAGGTGACCGGACTGGGGGACTGGGGGCTGGCTGGCGCTGGCG CCAACAGGTGACCGGACTGGGGGCTGGCTGGCGCTGGCGCTGGCG 360 370 380 390 400 410 420					
510 520 530 540 550 560 570 TGCTGGTTCACCTGGCACGGCTGGCTGGCTGGCTGGCTGGCC TGCTGGTTCACCTGGCACGGCTGGCTGGCTGGCTGGCC 500 510 520 530 540 550 560					
580 590 600 610 620 630 640 GGCGCGCGCTGTAACAGCTGGGGCTGGCCACTCAGGCCAGGCC GGCGCGCGCTGTAACAGCTGGGGCTGGCCACTCAGGCCAGGCC 570 580 590 600 610 620 630					
650 660 670 680 690 700 710 GTCCTGGGATGGGAACGGGGCTGGAACCATGGCTAGGGAGGGCG GTCCTGGGATGGGAACGGGGCTGGAACCATGGCTAGGGAGGGCG 650 660 670 680 690 700 710					

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2470 2480 2490 2500 2510
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